WHAT IS CLAIMED IS:

10. A method for identifying a polypeptide that binds to a peptide in a chosen protein, wherein said polypeptide is not an antibody, comprising:

(a) providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being attached to a support;

(b) contacting the support with a mixture of polypeptides under conditions enabling binding between the support and a polypeptide of the mixture;

(c) washing the support to remove unbound polypeptides of the mixture; and

(d) identifying the polypeptide that binds to the support;

wherein a polypeptide that binds to the support is the polypeptide that binds to the peptide in the chosen protein.

11. The method of claim 10, wherein the polypeptide that binds to the peptide in the chosen protein binds to a high affinity domain of the chosen protein.

12. The method of claim 10, wherein the support is selected from the group consisting of a chip, bead, and plate.

13. The method of claim 10, wherein the set of support-attached overlapping peptides is synthesized synthetically using the amino acid sequence of the chosen protein.

14. The method of claim 10, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 15 amino acids in length.

15. The method of claim 10, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 12 amino acids in length.

16. The method of claim 10, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 10 amino acids in length.

17. The method of claim 10, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 7 amino acids in length.

18. The method of claim 10, wherein the set of overlapping peptides is covalently attached to the support.

19. The method of claim 10, wherein the support is contacted with a lysate from a cell, wherein the lysate comprises the mixture of polypeptides.

20. The method of claim 10, wherein the chosen protein is human P-glycoprotein 1.

21. The method of claim 20, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 1, a second domain consisting of the amino acid sequence of SEQ ID NO: 2, a third domain consisting of the amino acid sequence of SEQ ID NO: 3, and a combination of the first, second, and third domains.

22. The method of claim 20, wherein the set of overlapping peptides comprises a first peptide consisting of an amino acid sequence of SEQ ID NO: 7 and a second peptide consisting of an amino acid sequence of SEQ ID NO: 8.

23. The method of claim 20, wherein the polypeptide is tubulin.

24. The method of claim 10, wherein the chosen protein is human P-glycoprotein 3.

25. The method of claim 24, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 4, a second domain consisting of the amino acid sequence of SEQ ID NO: 5, a third domain consisting of the amino acid sequence of SEQ ID NO: 6, and a combination of the first, second, and third domains.

26. A method for identifying a peptide in a chosen protein that binds to a polypeptide, wherein said polypeptide is not an antibody, the method comprising:

(a) providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being attached to a support;

(b) contacting the support with a polypeptide under conditions enabling binding between the support and the polypeptide;

(c) washing the support to remove unbound polypeptide; and

(d) identifying the peptide of the support that binds to the polypeptide.

27. The method of claim 26, wherein the peptide of the support that binds to the polypeptide is included within a high affinity domain of the chosen protein.

28. The method of claim 26, wherein the support is contacted with the mixture of polypeptides under conditions enabling binding between the support and the polypeptide of the mixture.

29. The method of claim 26, wherein the support is selected from the group consisting of a chip, bead, and plate.

30. The method of claim 26, wherein the set of support-attached overlapping peptides of the support is synthesized synthetically using the amino acid sequence of the chosen protein.

31. The method of claim 26, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 15 amino acids in length.

32. The method of claim 26, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 12 amino acids in length.

33. The method of claim 26, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 10 amino acids in length.

34. The method of claim 26, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 7 amino acids in length.

35. The method of claim 26, wherein the set of overlapping peptides is covalently attached to the support.

36. The method of claim 26, wherein the chosen protein is human P-glycoprotein 1.

37. The method of claim 36, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 1, a second domain consisting of the amino acid sequence of SEQ ID NO: 2, a third domain consisting of the amino acid sequence of SEQ ID NO: 3, and a combination of the first, second, and third domains.

38. The method of claim 36, wherein the set of overlapping peptides comprises a first peptide consisting of an amino acid sequence of SEQ ID NO:7 and a second peptide consisting of an amino acid sequence of SEQ ID NO:8.

39. The method of claim 36, wherein the polypeptide is tubulin.

40. The method of claim 26, wherein the chosen protein is human P-glycoprotein 3.

41. The method of claim 40, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 4, a second domain consisting of the amino acid sequence of SEQ ID NO: 5, a third domain consisting of the amino acid sequence of SEQ ID NO: 6, and a combination of the first, second, and third domains.

42. A method of identifying a compound that modulates the binding of a polypeptide to a peptide in a chosen protein, wherein said polypeptide is not an antibody, comprising:

(a) providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being attached to a support;

(b) contacting the support with a candidate compound and the polypeptide under conditions enabling binding between the support and the polypeptide;

(c) washing the support to remove unbound polypeptides of the mixture; and

(d) detecting binding of the polypeptide to the support;

wherein a change in the binding of the polypeptide to the support in the presence of the candidate compound compared to the binding of the polypeptide to the support in the absence of the candidate compound identifies the candidate compound as a compound that modulates binding of the polypeptide to the peptide in the chosen protein.

43. The method of claim 42, wherein the domain of the chosen protein is a high affinity domain of the chosen protein.

44. The method of claim 42, wherein the polypeptide is known to bind to the chosen protein.

45. The method of claim 42, wherein the support is selected from the group consisting of a chip, bead, and plate.

46. The method of claim 42, wherein the set of support-attached overlapping peptides of the support is synthesized synthetically using the amino acid sequence of the chosen protein.

47. The method of claim 42, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 15 amino acids in length.

48. The method of claim 42, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 12 amino acids in length.

49. The method of claim 42, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 10 amino acids in length.

50. The method of claim 42, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 7 amino acids in length.

51. The method of claim 42, wherein the set of overlapping peptides is covalently attached to the support.

52. The method of claim 42, wherein the chosen protein is human P-glycoprotein 1.

53. The method of claim 52, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 1, a second domain consisting of the amino acid sequence of SEQ ID NO: 2, a third domain consisting of the amino acid sequence of SEQ ID NO: 3 and a combination of the first, second, and third domains.

54. The method of claim 52, wherein the set of overlapping peptides comprises a first peptide consisting of an amino acid sequence of SEQ ID NO: 7 and a second peptide consisting of an amino acid sequence of SEQ ID NO: 8.

55. The method of claim 52, wherein the polypeptide is tubulin.

56. The method of claim 42, wherein the chosen protein is human P-glycoprotein 3.

57. The method of claim 56, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 4, a second domain consisting of the amino acid sequence of SEQ ID NO: 5, a third domain consisting of the amino acid sequence of SEQ ID NO: 6, and a combination of the first, second, and third domains.

58. A support to which is attached a set of overlapping peptides spanning a complete sequence of at least a domain of a protein.

59. The support of claim 58, wherein the domain of the protein is a high affinity domain of the protein.

60. The support of claim 58, wherein set of overlapping peptides spans the complete sequence of the entire protein.

61. The support of claim 58, wherein the support is selected from the group consisting of a chip, bead, and plate.

62. The support of claim 58, wherein the set of support-attached overlapping peptides of the support is synthesized synthetically using the amino acid sequence of the chosen protein.

63. The support of claim 58, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 15 amino acids in length.

64. The support of claim 58, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 12 amino acids in length.

65. The support of claim 58, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 10 amino acids in length.

66. The support of claim 58, wherein each of the peptides in the set of support-attached overlapping peptides is from about 5 amino acids to about 7 amino acids in length.

67. The support of claim 58, wherein the set of overlapping peptides is covalently attached to the support.

68. The support of claim 58, wherein a polypeptide that binds to a peptide attached to the support is identified as a polypeptide that binds to the protein.

69. The support of claim 58, wherein the chosen protein is human P-glycoprotein 1.

70. The support of claim 69, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 1, a second domain

consisting of the amino acid sequence of SEQ ID NO: 2, a third domain consisting of the amino acid sequence of SEQ ID NO: 3, and a combination of the first, second, and third domains.

71. The support of claim 69, wherein the set of overlapping peptides comprises a first peptide consisting of an amino acid sequence of SEQ ID NO:7 and a second peptide consisting of an amino acid sequence of SEQ ID NO: 8.

72. The support of claim 58, wherein the chosen protein is human P-glycoprotein 3.

73. The support of claim 72, wherein the domain is selected from the group consisting of a first domain consisting of the amino acid sequence of SEQ ID NO: 4, a second domain consisting of the amino acid sequence of SEQ ID NO: 5, a third domain consisting of the amino acid sequence of SEQ ID NO: 6, and a combination of the first, second, and third domains.

74. A method for purifying tubulin comprising:

a) contacting a sample containing tubulin with a support to which is attached a first peptide consisting of an amino acid sequence of RSSLIR and a second peptide consisting of an amino acid sequence of SVRGSQ, wherein the contacting is under conditions enabling binding between the support and the tubulin in the same;

b) rinsing the sample-contacted support to remove unbound molecules in said sample; and

c) eluting said tubulin bound to said support;

wherein said tubulin eluted from said support is purified.